Sequence Search (handwritten)

OM protein - protein search, using sw model

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

Run on: September 12, 2005, 19:28:11 ; Search time 161 Seconds
(without alignments)
48.998 Million cell updates/sec

Title: US-09-777-560-1
Perfect score: 90
Sequence: 1 RRKKAAVALLPAVLLALLAP 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1777461 seqs, 39431504 residues

Total number of hits satisfying chosen parameters: 1777461

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Database : Published Applications AA:*
1: /cgn2_6/ptcdata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptcdata/2/pubpaa/US09C_PUBCOMB.pep:*
3: /cgn2_6/ptcdata/2/pubpaa/PCT_NEW_PUB.pep:*
4: /cgn2_6/ptcdata/2/pubpaa/US06_NEW_PUB.pep:*
5: /cgn2_6/ptcdata/2/pubpaa/US06_PUBCOMB.pep:*
6: /cgn2_6/ptcdata/2/pubpaa/US07_NEW_PUB.pep:*
7: /cgn2_6/ptcdata/2/pubpaa/PCTUS_PUBCOMB.pep:*
8: /cgn2_6/ptcdata/2/pubpaa/US08_NEW_PUB.pep:*
9: /cgn2_6/ptcdata/2/pubpaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptcdata/2/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptcdata/2/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptcdata/2/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptcdata/2/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptcdata/2/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptcdata/2/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptcdata/2/pubpaa/US10D_PUBCOMB.pep:*
17: /cgn2_6/ptcdata/2/pubpaa/US10E_PUBCOMB.pep:*
18: /cgn2_6/ptcdata/2/pubpaa/US10_NEW_PUB.pep:*
19: /cgn2_6/ptcdata/2/pubpaa/US11_NEW_PUB.pep:*
20: /cgn2_6/ptcdata/2/pubpaa/US11A_PUBCOMB.pep:*
21: /cgn2_6/ptcdata/2/pubpaa/US60_NEW_PUB.pep:*
22: /cgn2_6/ptcdata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	90	100.0	20	12	US-09-777-560-1	Sequence 1, Appli
2	90	100.0	20	12	US-09-777-560-2	Sequence 2, Appli
3	80	88.9	29	15	US-10-126-103-124	Sequence 124, App
4	80	88.9	29	15	US-10-431-096-124	Sequence 124, Appl
5	80	88.9	29	17	US-10-858-367-60	Sequence 60, Appl
6	75	83.3	17	12	US-09-777-560-27	Sequence 27, Appl
7	72.5	80.6	20	12	US-09-777-560-3	Sequence 3, Appli
8	70	77.8	16	9	US-09-214-371-45	Sequence 45, Appl
9	70	77.8	16	9	US-09-811-870-5	Sequence 5, Appli
10	70	77.8	16	9	US-09-785-802a-9	Sequence 9, Appli
11	70	77.8	16	10	US-09-962-967A-3	Sequence 3, Appli
12	70	77.8	16	10	US-09-965-876A-3	Sequence 3, Appli
13	70	77.8	16	10	US-09-789-831-12	Sequence 12, Appl
14	70	77.8	16	14	US-10-226-956-285	Sequence 285, App
15	70	77.8	16	14	US-10-077-555-7	Sequence 7, Appl
16	70	77.8	16	14	US-10-211-088-303	Sequence 303, App
17	70	77.8	16	14	US-10-136-738-18	Sequence 18, Appl
18	70	77.8	16	14	US-10-156-570A-26	Sequence 26, Appl
19	70	77.8	16	15	US-10-144-549-18	Sequence 18, Appl
20	70	77.8	16	15	US-10-185-593-4	Sequence 4, Appli
21	70	77.8	16	15	US-10-232-410-1	Sequence 1, Appli
22	70	77.8	16	15	US-10-826-181-22	Sequence 22, Appl
23	70	77.8	16	15	US-10-465-826-27	Sequence 27, Appl
24	70	77.8	16	15	US-10-751-380-7	Sequence 7, Appl
25	70	77.8	16	15	US-10-688-299-18	Sequence 18, Appl
26	70	77.8	16	15	US-10-722-176A-6	Sequence 6, Appli
27	70	77.8	16	15	US-10-722-176A-9	Sequence 9, Appli
28	70	77.8	16	15	US-10-148-457A-5	Sequence 5, Appli
29	70	77.8	16	16	US-10-823-259-37	Sequence 37, Appl
30	70	77.8	16	17	US-10-823-254-37	Sequence 37, Appl
31	70	77.8	16	17	US-10-916-185-16	Sequence 16, Appl
32	70	77.8	16	17	US-10-700-971C-7	Sequence 7, Appl
33	70	77.8	16	18	US-10-927-262A-45	Sequence 45, Appl
34	70	77.8	16	18	US-10-319-316-5	Sequence 5, Appli
35	70	77.8	16	18	US-10-878-175B-37	Sequence 37, Appl
36	70	77.8	16	18	US-10-991-286A-46	Sequence 46, Appl
37	70	77.8	16	19	US-11-027-967-4	Sequence 4, Appli
38	70	77.8	16	20	US-10-004-795A-117	Sequence 117, App
39	70	77.8	16	20	US-11-004-379-22	Sequence 22, Appl
40	70	77.8	16	17	US-09-777-560A-101	Sequence 101, App
41	70	77.8	16	18	US-11-066-697-1058	Sequence 1058, App
42	70	77.8	20	12	US-09-777-560-19	Sequence 19, App
43	70	77.8	20	14	US-11-066-697-1060	Sequence 1060, Ap
44	70	77.8	20	14	US-11-136-738-45	Sequence 45, Ap
45	70	77.8	22	16	US-10-688-299-45	Sequence 45, Appl

ALIGNMENTS

RESULT 1
US-09-777-560-1
Sequence 1, Application US/09777560
Publication No. US20050130884A1

GENERAL INFORMATION:
US-09-777-560-1

APPLICANT: BRANDT, CURTIS R.
APPLICANT: BULTMANN, HERMANN
TITLE OF INVENTION: PHARMACOLOGICALLY ACTIVE ANTIVIRAL PEPTIDES AND METHODS
TITLE OF INVENTION: OF THEIR USE
FILE REFERENCE: 03206-0460
CURRENT APPLICATION NUMBER: US/09/777,560
CURRENT FILING DATE: 2001-02-06
PRIOR APPLICATION NUMBER: 60/184,057
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: 60/180,823
PRIOR FILING DATE: 2000-02-07
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin Ver. 3.2

SEQ ID NO 1
LENGTH: 20
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: peptide
US-09-777-560-1

Query Match 100.0%; Score 90; DB 12; Length 20;
Best Local Similarity 100.0%;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRKKAAVALLPAVLLALLAP 20
       ||||||||||||||||||||
Db 1 RRKKAAVALLPAVLLALLAP 20

Pred. No. 2.6e-06;

OM protein - protein search, using sw model

Copyright (c) 1993 - 2005 Compugen Ltd.

GenCore version 5.1.6

Run on: September 12, 2005, 19:19:20 ; Search time 42 Seconds
(without alignments)
35.547 Million cell updates/sec

Title: US-09-777-560-1
Perfect score: 90
Sequence: 1 RRKKAAVALLPAVLLALLAP 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	80	88.9	29	2	US-08-928-958-24	Sequence 24, Appl
2	80	88.9	29	2	US-09-072-429-24	Sequence 24, Appl
3	80	88.9	30	2	US-08-928-958-1	Sequence 1, Appl
4	80	88.9	30	2	US-09-072-429-1	Sequence 1, Appli
5	70	77.8	16	1	US-08-642-493-1	Sequence 1, Appli
6	70	77.8	16	1	US-08-258-852-5	Sequence 5, Appli
7	70	77.8	16	2	US-08-928-958-4	Sequence 4, Appli
8	70	77.8	16	2	US-09-072-429-4	Sequence 4, Appli
9	70	77.8	16	3	US-08-964-302A-3	Sequence 3, Appli
10	70	77.8	16	4	US-10-116-288A-23	Sequence 23, Appl
11	70	77.8	16	3	US-09-170-754B-5	Sequence 5, Appl
12	70	77.8	16	3	US-09-441-416A-3	Sequence 3, Appli
13	70	77.8	16	3	US-09-230-548-19	Sequence 19, Appl
14	70	77.8	16	4	US-09-230-548-19	Sequence 19, Appl
15	70	77.8	16	4	US-09-935-032-1	Sequence 1, Appli
16	70	77.8	16	4	US-10-083-889-7	Sequence 7, Appli
17	70	77.8	16	4	US-10-083-889-7	Sequence 7, Appli
18	70	77.8	16	4	US-10-116-288A-23	Sequence 23, Appl
19	70	77.8	16	5	US-10-144-549-18	Sequence 18, Appl
20	70	77.8	24	3	PCT-US95-07539-5	Sequence 5, Appl
21	70	77.8	25	1	US-09-230-548-21	Sequence 21, Appl
22	70	77.8	26	1	US-08-258-852-1	Sequence 1, Appli
23	70	77.8	26	1	US-08-258-852-8	Sequence 8, Appli
24	70	77.8	26	1	US-08-258-852-3	Sequence 3, Appli
25	70	77.8	26	1	US-08-258-852-9	Sequence 9, Appli
26	70	77.8	26	2	US-08-928-958-2	Sequence 2, Appli
27	70	77.8	26	2	US-08-928-958-5	Sequence 5, Appli
28	70	77.8	26	2	US-09-072-429-2	Sequence 2, Appli
29	70	77.8	26	2	US-09-072-429-5	Sequence 5, Appl
30	70	77.8	26	3	US-09-170-754B-1	Sequence 1, Appl
31	70	77.8	26	3	US-09-170-754B-3	Sequence 3, Appli
32	70	77.8	26	3	US-09-170-754B-8	Sequence 8, Appli
33	70	77.8	26	3	US-09-170-754B-9	Sequence 9, Appli
34	70	77.8	26	4	US-09-450-071A-1	Sequence 1, Appli
35	70	77.8	26	4	US-09-450-071A-3	Sequence 3, Appli
36	70	77.8	26	4	US-09-450-071A-8	Sequence 8, Appli
37	70	77.8	26	4	US-09-450-071A-9	Sequence 9, Appli
38	70	77.8	26	4	US-09-450-071A-13	Sequence 13, Appl
39	70	77.8	26	5	US-09-997-465B-1	Sequence 1, Appl
40	70	77.8	26	5	PCT-US95-07539-1	Sequence 1, Appli
41	70	77.8	26	5	PCT-US95-07539-3	Sequence 3, Appli
42	70	77.8	26	5	PCT-US95-07539-8	Sequence 8, Appli
43	70	77.8	26	5	PCT-US95-07539-9	Sequence 9, Appli
44	70	77.8	28	1	US-08-258-852-4	Sequence 4, Appli
45	70	77.8	28	3	US-09-170-754B-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-08-928-958-24
Sequence 24, Application US/08928958
Patent No. 5877282

GENERAL INFORMATION:
APPLICANT: NADLER, STEVEN G.
APPLICANT: CLEAVELAND, JEFFREY S.
APPLICANT: BLAKE, JAMES
APPLICANT: HAFFAR, OMAR K.
TITLE OF INVENTION: PEPTIDE INHIBITORS OF NUCLEAR PROTEIN
TITLE OF INVENTION: TRANSLOCATION HAVING NUCLEAR LOCALIZATION SEQUENCES AND
TITLE OF INVENTION: METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: ROBINS & ASSOCIATES
STREET: 90 MIDDLEFIELD ROAD, SUITE 200
CITY: MENLO PARK
STATE: CA
COUNTRY: USA
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,958
FILING DATE: 12-SEP-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/026978
FILING DATE: 20-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: ROBINS, ROBERTA L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 5998-0019
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 325-7812
TELEFAX: (650) 325-7823
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide

US-08-928-958-24
Query Match 88.9%; Score 80; DB 2; Length 29;
Best Local Similarity 90.0%; Pred. No. 1.2e-05;

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 12, 2005, 19:29:47 ; Search time 167 Seconds
(without alignments)
61.327 Million cell updates/sec

Title:
Perfect score: 90
Sequence: 1 RRKKAAVALLPAVLLALLAP 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Total number of hits satisfying chosen parameters: 1612378

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

ult No.	Score	% Match	Query Length	DB	ID	Description
1	70	77.8	206	1	P08620	homo sapien
2	63	70.0	206	1	P48803	bos taurus
3	55	61.1	74	2	Q9HRE2	halobacteri
4	53	58.9	100	2	Q92R04	rhizobium m
5	51.5	57.2	450	1	ACHX_HUMAN	homo sapien
6	50	55.6	177	2	Q8Y713	listeria mo
7	50	55.6	177	2	CADM_HUMAN	homo sapien
8	49	54.4	177	2	Q720F8	listeria mo
9	49	54.4	194	2	FGF4_CHICK	gallus gall
10	49	54.4	205	2	Q9KZV1	streptomyce
11	49	54.4	346	2	Q6W2C3	rhizobium s
12	49	54.4	488	1	P24347	homo sapien
13	49	54.4	488	1	MM11_HUMAN	homo sapien
14	48	53.3	167	2	O6PEZ6	mycobacteri
15	48	53.3	167	2	O53527	mycobacteri
16	48	53.3	340	2	Q7VEM9	pseudomonas
17	48	53.3	417	1	O88PY1	pseudomonas
18	48	53.3	468	2	MUA2_CLOPE	clostridium
19	48	53.3	529	2	Q6M576	mycoplasma
20	47.5	52.8	447	2	O8CNA8	staphylococ
21	47	52.2	285	2	Q9JLB5	rattus norv
22	47	52.2	285	2	O72FG9	desulfovibr
23	47	52.2	286	2	O9RDG2	streptomyce
24	47	52.2	317	2	Q91174	pseudomonas
25	47	52.2	328	2	O48W5	bacillus me
26	47	52.2	407	2	O89MR3	bradyrhizob
27	47	52.2	428	2	O8EM55	oceanobacil
28	47	52.2	551	2	O8WOB2	oryza sativ
29	47	52.2	202	2	O9RU46	deinococcus
30	46	51.1	252	2	O7NTD4	chromobacte
31	46	51.1	267	2	O8PIV1	xanthomonas
32	46	51.1	417	1	MUA3_THETN Q8r6v0	agrobacteri / thermoanaer
33	46	51.1	418	2	MUA2_CIOAB Q97dd9	clostridium
34	46	51.1	431	2	Q9AM70	rhodospiril
35	46	51.1	601	2	Q82RB2	streptomyce
36	45	50.0	100	2	Q82EE2	streptomyce
37	45	50.0	217	2	Q8UGF5	agrobacteri
38	45	50.0	255	2	Q82N19	streptomyce
39	45	50.0	289	2	Q9LIY6	oryza sativ
40	45	50.0	289	2	Q8VQ63 MUA2_STAAM	
41	45	50.0	419	1	Q8VG63 MUA2_STAAN	
42	45	50.0	419	1	Q65FH4 MUA2_STAAN	
43	45	50.0	419	1	P65457 MUA2_STAAW	
44	45	50.0	419	1	P65456	bacillus li
45	45	50.0	419	2	Q6G7I6	staphylococ

ALIGNMENTS

RESULT 1
```
ID   FGF4_HUMAN
     FGF4_HUMAN     STANDARD;     PRT;   206 AA.
AC   P08620;
DT   01-AUG-1988 (Rel. 08, Created)
DT   01-AUG-1988 (Rel. 08, Last sequence update)
DT   25-OCT-2004 (Rel. 45, Last annotation update)
DE   Fibroblast growth factor-4 precursor (FGF-4) (Heparin secretory
DE   transforming protein) (HST) (Transforming protein KS3) (HBGP-
DE   4).
GN   Name=FGF4; Synonyms=HST, HSTF1, KS3;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=88041096; PubMed=2959959;
RA   Yoshida T., Miyagawa K., Odagiri H., Sakamoto H., Little P.F.R.,
RA   Terada M., Sugimura T.;
RT   "Genomic sequence of hst, a transforming gene encoding a protein
RT   homologous to fibroblast growth factors and the int-2-encoded
RT   protein.";
RL   Proc. Natl. Acad. Sci. U.S.A. 84:7305-7309(1987).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=87204251; PubMed=2953031;
RA   Taira M., Yoshida T., Miyagawa K., Sakamoto H., Terada M.,
RA   Sugimura T.;
RT   "cDNA sequence of human transforming gene hst and identification of
RT   the coding sequence required for transforming activity.";
RL   Proc. Natl. Acad. Sci. U.S.A. 84:2980-2984(1987).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=87301716; PubMed=2957062; DOI=10.1016/0092-8674(87)90331-X;
RA   Delli Bovi P., Curatola A.M., Kern F.G., Greco A., Ittmann M.,
RA   Basilico C.;
RT   "An oncogene isolated by transfection of Kaposi's sarcoma DNA encodes
RT   a growth factor that is a member of the FGF family.";
RL   Cell 50:729-737(1987).
RN   [4]
RP   X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 79-206.
RX   PubMed=11486033; DOI=10.1128/MCB.21.17.5946-5957.2001;
RA   Bellosta P., Iwahori A., Plotnikov A.N., Eliseenkova A.V.,
RA   Basilico C., Mohammadi M.;
RT   "Identification of receptor and heparin binding sites in fibroblast
RT   growth factor 4 by structure-based mutagenesis.";
RL   Mol. Cell. Biol. 21:5946-5957(2001).
CC   -!- FUNCTION: Can transform NIH 3T3 cells from a human stomach tumor
CC       (hst) and from Kaposi's sarcoma (KS3). It has a mitogenic
CC       activity.
CC   -!- SIMILARITY: Belongs to the heparin-binding growth factors family.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
```

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 12, 2005, 19:38:07 ; Search time 39 Seconds
(without alignments)
49.342 Million cell updates/sec

Title: US-09-777-560-1
Perfect score: 90
Sequence: 1 RRKAAVALLPAVLLALLAP 20
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79.*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	70	77.8	206	1	TVHHS	fibroblast growth
2	63	70.0	206	2	JC6268	fibroblast growth
3	55	61.1	74	2	D84231	hypothetical prote
4	50	55.6	177	2	AH1232	hypothetical prote
5	49	54.4	194	2	I50710	fibroblast growth
6	49	54.4	488	2	S13423	fibroblast growth
7	48	53.3	167	2	A70862	stromelysin 3 (EC
8	47	52.2	317	2	B83344	hypothetical prote
9	46	51.1	202	2	D75583	probable adhesion
10	46	51.1	353	2	AH3116	conserved hypothet
11	46	51.1	353	2	E98170	transcription regu
12	46	51.1	418	2	E99334	UDP-N-acetylglucos
13	46	51.1	1251	2	A57293	latent transformin
14	45	50.0	100	2	C97492	hypothetical prote
15	45	50.0	100	2	AB2710	conserved hypothet
16	45	50.0	419	2	A99906	hypothetical prote
17	45	50.0	423	2	AH1393	UDP-N-acetylglucos
18	45	50.0	423	2	AC1769	UDP-N-acetylglucos
19	45	50.0	428	2	H84122	UDP-N-acetylglucos
20	45	50.0	429	2	G32354	UDP-N-acetylglucos
21	45	50.0	441	2	S4710	mitosis-specific c
22	45	50.0	556	2	T4842	K+-transporting At
23	45	50.0	557	2	H97351	K+-transporting At
24	45	50.0	858	2	T08881	prominin - mouse
25	44	48.9	244	2	S36245	chaperone-like pro
26	44	48.9	244	2	JC8019	CD58 protein - pig
27	44	48.9	419	2	A95125	hypothetical prote
28	44	48.9	419	2	B97995	UDP-N-acetylglucos
29	44	48.9	512	2	E83060	iron (III)-transpo
30	44	48.9	534	2	P90031	PTS system, arbuti
31	44	48.9	917	2	B81309	isoleucine-tRNA li
32	44	48.9	1094	2	P70697	probable arabinosy
33	44	48.9	5376	2	T42215	zonadhesin - mouse
34	44	47.8	120	2	T44554	hypothetical prote
35	43	47.8	221	2	B86200	hypothetical prote
36	43	47.8	334	2	G84123	iron (III) dicitra
37	43	47.8	494	2	AC0133	probable permease
38	43	47.8	660	2	B85499	probable permease
39	43	47.8	660	2	B90648	hypothetical prote
40	43	47.8	660	2	A64739	ferrichrome-iron t
41	43	47.8	1230	2	S47466	cellulose 1,4-beta
42	42.5	47.2	1308	2	T15280	hypothetical prote
43	42	47.2	219	2	A80945	probable exported
44	42	46.7	253	2	G71560	probable sigma-28/
45	42	46.7	256	2	T35133	hypothetical prote

ALIGNMENTS

RESULT 1
TVHHS
TVHHS
fibroblast growth factor 4 - human
N;Alternate names: heparin secretory transforming protein 1; Kaposi sarcoma oncogene;
C;Species: Homo sapiens (man)
C;Date: 31-Mar-1989 #sequence revision 31-Mar-1989 #text_change 09-Jul-2004
C;Accession: A28417; A29876; A29649
R;Yoshida, T.; Miyagawa, K.; Odagiri, H.; Sakamoto, H.; Little, P.F.R.; Terada, M.; Su
Proc. Natl. Acad. Sci. U.S.A. 84, 7305-7309, 1987
A;Title: Genomic sequence of hst, a transforming gene encoding a protein homologous to
A;Reference number: A28417; MUID:88041096; PMID:2959959
A;Accession: A28417
A;Molecule type: DNA
A;Residues: 1-206 <YOS>
A;Cross-references: UNIPROT:P08620; DDBJ:J02986; GB:M16338; NID:g184430; PIDN:AAB59555.1; PID:g38
R;Taira, M.; Yoshida, T.; Miyagawa, K.; Sakamoto, H.; Terada, M.; Sugimura, T.
Proc. Natl. Acad. Sci. U.S.A. 84, 2980-2984, 1987
A;Title: cDNA sequence of human transforming gene hst and identification of the coding
A;Reference number: A29876; MUID:87204251; PMID:2953031
A;Accession: A29876
A;Molecule type: mRNA
A;Residues: 1-206 <TAI>
A;Cross-references: GB:J02986; GB:M16338; NID:g184431; PIDN:AAB59555.1; PID:g386788
R;Delli Bovi, P.; Curatola, A.M.; Kern, F.G.; Greco, A.; Ittmann, M.; Basilico, C.
Cell 50, 729-737, 1987
A;Title: An oncogene isolated by transfection of Kaposi's sarcoma DNA encodes a growth
A;Reference number: A29649; MUID:87301716; PMID:2957062
A;Accession: A29649
A;Molecule type: mRNA
A;Residues: 1-206 <BOV>
A;Cross-references: GB:M17446; NID:g186785; PIDN:AAA59473.1; PID:g307092
C;Comment: This protein is an oncogene for Kaposi's sarcoma. It is homologous to the m
C;Genetics:
A;Gene: GDB:FGF4; HSTF1
A;Cross-references: GDB:120066; OMIM:164980
A;Map position: 11q13.3-11q13.3
A;Introns: 114/1; 148/3
C;Superfamily: fibroblast growth factor; Kaposi sarcoma; transforming protein
C;Keywords: growth factor; Kaposi sarcoma; transforming protein

```
Qy      5 AAVALLPAVLLALLAP 20
          ||||||||||||||||
Db      7 AAVALLPAVLLALLAP 22
```

Query Match 77.8%; Score 70; DB 1; Length 206;
Best Local Similarity 100.0%; Pred. No. 0.0038;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 2
JC4268
fibroblast growth factor 4 - bovine

OM protein - protein search, using sw model

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

Run on: September 12, 2005, 19:29:07 ; Search time 164 Seconds
                                                (without alignments)
                                                47.166 Million cell updates/sec

Title: US-09-777-560-1
Perfect score: 90
Sequence: 1 RRKKAAVALLPAVLLALLAP 20
Scoring table: 1
Searched: 2105692 seqs, 386760381 residues
Scoring table: BLOSUM62
                   Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                   Maximum Match 100%
                   Listing first 45 summaries

Database :   A_Geneseq_16Dec04:*
                   1: geneseqp1980s:*
                   2: geneseqp1990s:*
                   3: geneseqp2000s:*
                   4: geneseqp2001s:*
                   5: geneseqp2002s:*
                   6: geneseqp2003ss:*
                   7: geneseqp2003bs:*
                   8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	% Length	DB	ID	Description
1	90	100.0	20	4	AAB12478	Aae12478 Membrane
2	90	100.0	20	4	AAB12477	Aae12477 Membrane
3	84	93.3	20	4	AAY67963	Aay67963 Karposi s
4	84	93.3	22	3	AAY67959	Aay67959 Karposi s
5	82	91.1	19	3	AAY67956	Aay67956 Karposi s
6	82	91.1	22	3	AAY67958	Aay67958 Karposi s
7	80	88.9	29	3	AAY55835	Aay55835 SV40MEM p
8	80	88.9	29	6	AAY55835	Aay55835 SV40MEM p
9	80	88.9	30	2	ABU69594	Abu69594 Human NF-
10	80	88.9	30	3	AAW56391	Aaw56391 SV40MEM p
11	75	83.3	17	3	AAY55812	Aay55812 SV40MEM p
12	75	83.3	17	4	AAY67961	Aay67961 Karposi s
13	75	83.3	20	3	AAE12503	Aae12503 Membrane
14	75	83.3	20	4	AAY67962	Aay67962 Karposi s
15	75	83.3	27	4	AAY72146	Aay72146 Anti-alle
16	73	81.1	29	2	AAY72145	Aay72145 Anti-alle
17	72.5	80.6	20	4	AAW56414	Aaw56414 Nuclear t
18	70	77.8	16	2	AAE12479	Aae12479 Membrane
19	70	77.8	16	2	AAR87629	Aar87629 Signal pe
20	70	77.8	16	2	AAW37753	Aaw37753 Chimeric
21	70	77.8	16	2	AAW56394	Aaw56394 MEM polyp
22	70	77.8	16	2	AAW48689	Aaw48689 Signal pe
23	70	77.8	16	2	AAW37769	Aaw37769 PKR pepti
24	70	77.8	16	2	AAY13506	Aay13506 Signal se
25	70	77.8	16	3	AAY67954	Aay67954 Karposi s
26	70	77.8	16	4	AAY55815	Aay55815 Fibroblas
27	70	77.8	16	4	AAU97005	Aau97005 CCAAT enh
28	70	77.8	16	4	AAE11949	Aae11949 Membrane
29	70	77.8	16	4	AAU03154	Aau03154 Peptide K
30	70	77.8	16	4	AAY72476	Aay72476 Kaposi fi
31	70	77.8	16	4	ABG78989	Abg78989 Cell pene
32	70	77.8	16	5	AAU10399	Aau10399 Membrane
33	70	77.8	16	5	AAB15613	Aab15613 Kaposi's
34	70	77.8	16	5	AAU78349	Aau78349 Signal se
35	70	77.8	16	5	AAE26128	Aae26128 Kaposi fi
36	70	77.8	16	5	ABG75507	Abg75507 Signal-se
37	70	77.8	16	5	ABB81177	Abb81177 Fluoresce
38	70	77.8	16	5	AAE23686	Aae23686 Signal se
39	70	77.8	16	5	ABB82543	Abb82543 Signal se
40	70	77.8	16	5	ABR84444	Abr84444 K-FGF sig
41	70	77.8	16	6	AAE33897	Aae33897 Kaposi's
42	70	77.8	16	6	ABU09984	Abu09984 Kaposi's
43	70	77.8	16	6	ADC22454	Adc22454 Protein-d
44	70	77.8	16	7	ADF78064	Adf78064 Human mem
45	70	77.8	16	7	ADG28017	Adg28017 Kaposi FG

ALIGNMENTS

RESULT 1
AAB12478

ID   AAB12478 standard; peptide; 20 AA.
XX
AC   AAB12478;
XX
DT   03-JAN-2002 (first entry)
XX
DE   Membrane transiting antiviral peptide bBB.
XX
KW   Membrane transiting peptide; virucide; antiviral; Herpes Simplex Virus;
KW   HSV; HIV; Human Immunodeficiency Virus; CMV; cytomegalovirus.
XX
OS   Unidentified.
XX
FH   Key   Location/Qualifiers
FT   Modified-site   1
FT   /note= "Biotin-aminohexanoyl Arg"
XX
PN   WO200157072-A2.
XX
PD   09-AUG-2001.
XX
PF   06-FEB-2001; 2001WO-US003813.
XX
PR   07-FEB-2000; 2000US-0180822P.
PR   22-FEB-2000; 2000US-0184057P.
XX
PA   (WISC) WISCONSIN ALUMNI RES FOUND.
XX
PI   Brandt C, Bultmann H;
XX
DR   WPI; 2001-638840/73.
XX
PT   Peptides comprising membrane transiting peptides useful for treating or
PT   preventing a virus infection, e.g., human immunodeficiency virus, herpes
PT   simplex virus and cytomegalovirus.
XX
PS   Claim 7; Page 15; 43pp; English.
XX
CC   The invention relates to peptides comprising membrane transiting peptides
CC   with antiviral properties. The peptides are useful for treating or
CC   preventing a virus infection in a warm blooded animal, e.g., enveloped
CC   viruses such as human immunodeficiency virus (HIV), herpes simplex virus
CC   (HSV), cytomegalovirus (CMV) and non-enveloped virus. Preferably, the
CC   peptides are useful for treating or preventing infections from one or
CC   more HSVs. The antiviral peptides are used for treating viral infections
CC   of the skin or part of the oral or genital cavity. The present sequence